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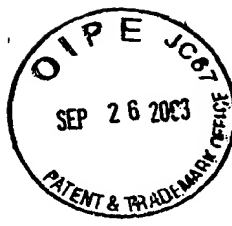
1/15

1 GNTCTAGAANTA GTGGATCCCCC GGGTGCGAGGAA TTCCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
 CNAGATCTTNAT CACCTAGGGGG CCCGACGTCTT AAGGTGCCGGG GACCTTCCCGAG ACCACCCCGACT
 73 GCGCTCTGCCG GGGGCGCGGGG ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGGCA TCAGCTACCCGG
 CGCGAGACGGG CCCCCGCGCCG TGTCGTCTTCG TCCAGGCGCACC CGCGACCCCGT AGTCGATGGCCC
 145 GTGTCGGGCT GAAGAGCCAGG AGCCAAGGCAGC CACCCCGGGGG TGGCGACCTTG GGGAGTTGGTG
 CACCAGGCCCGA CTTCTCGTCCG TCGTTCCGTCG GTGGGGCCCCC ACCCGCTGAAAC CCCCTCAACCAC
 217 CCCCCCCCCA GGCTTGCGGG GTCATGGGGCCC CCCCATTCTGG CCGGGGGCGGTG CGAGTCGGGGCC
 GGGCGGGGGT CCGGAACCGCCC CAGTACCCCGG MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla
 1 289 CTGCTGCTGCTG GGGGTTTGGG CTGGTGTCTGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
 GACGACGACGAC CCCCCAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA
 16 LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn
 361 AAGAGGTTCCAG GCAGAGGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
 TTCTCCAAGGTC CGTCTCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG
 40 LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro
 433 CGGGCCCCGCCT CCTGGCCCTCAC TCCTCTCCCTAAT TATGAGTTCTAC AAGCTGTACCCTG GTAGGGGGTGCT
 GCCCGGGCCGGA GGACCGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA
 64 ArgAlaArgPro ProGlyProHis SerSerProAsn TryGluPheTyr LysLeuTyrLeu ValGlyGlyAla
 505 CAGGGCCGGCGC TGTAGGCACCC CCTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCA GACCTGGATCTC
 GTCCCGGCGCGG ACACCTCGTGGG GGACGGGGTTG GAGGAAGAGTGA ACACCTAGCGGGT CTGGACCTAGAG
 88 GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu
 577 CGCTTACCATC AAGTTCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTCCGCTCG CACCACGATTAC
 GCGAAGTGGTAG TTCAAGGTCCTC ATATCGGGATTA GAGACCCCGGTG CTCGAAGCGGAGC GTGGTGCTAATG
 112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr

FIG. 1A

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169 TACATCATTGCC ACATCGGATGGG ACCGGGAGGGC CTGGAGAGCCTG CAGGGAGGTGTG TGCCTAACCAGA
 ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
 136 TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg
 721 GGCATGAAGGTG CTTCTCCAGTG GGACAAAGTCCC CGAGGAGGGGT GTCCCCCGAAAA CCTGTGTCTGAA
 CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCCTCCCGA CAGGGGCTTTT GGACACAGACTT
 160 GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu
 793 ATGCCCATGGAA AGAGACCGAGGG GCAGCCCCACAGC CTGGAGCCTGGG AAGGAGAACCTG CCAGGTGACCCC
 TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTG GACCTCGGACCC TTCCTCTTGGAC GGTCCACTGGGG
 184 MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro
 865 ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCTGCA GTGGCTGGGGCA
 TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCGT
 208 ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla
 937 GCAGGGGGGCTG GCGTGCTCTTG CTGGCGGTGGCA GGGGTGGGGT GCCATGTGTTGG CGGAGACGGCGG
 CGTCCCCCGAC CGCGACGAGAAC GACCCGCACCGT CCGCGACCCCA CGGTACACAACC GCCTCTGCCGCC
 232 AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg
 1009 GCCAAGCCTTCG GAGAGTCGCCAC CCTGGTCTTGG TCCTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGGT
 CGGTTCCGAAGC CTCTCAGCGGTG GGACCAGGACCG AGGAAGCCCTCC CCTCCACAGAGC CCGACCCCCCA
 256 AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly
 1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGGT GCGGGGGCTGCA
 CCTCCACCCCTAC CCTGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
 280 GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla
 1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGGG CATCCTGTGTAT ATCGTGCAGGAT
 CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCTTA
 304 AspProProphe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp
 1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACACA TCGATTTCTGTG TTGGAGTGGCCC ATATTGCATACG
 CCGGGGGGGTC TCGGAGGTTTG TAGATGATGTGT AGCTAAAGACAC AACCTCACCGGG TATAACGTATGC
 328 GlyProProGln SerProProAsn IleTyrTyrThr SerIleSerVal LeuGluTrpPro IleLeuHisThr

FIG. 1B

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1297 ATACAACTGTTT TTCAATCGGATCC AAGTGCTCCCGT GTCACATACATTC TTATTTCCCTGTG CAAGTTATTACG
 TATGTTGACAAA AAGTACGCTAGG TTCACGAGGGCA CAGTGATGTAAG AATAAAGGACAC GTTCAATAATGC
 352 IleGlnLeuPhe PheMetArgSer LysCysSerArg ValThrThrPhe LeuPheProVal GlnValIleThr
 1369 ACATCGACTTGC CGGATGACTTCA TTTAGCTTTACC ACCCTGAACCCA TCCATGCAGGCC TGCAGAGCACAG
 TGAGCTGAACG GCCTACTGAAGT AAATCGAAATGG TGGGACTTGGGT AGGTACGTCCGG ACGTCTCGTGTC
 376 ThrSerThyCys ArgMetThrSer PheSerPheThr ThrLeuAsnPro SerMetGlnAla CysArgAlaGln
 1441 ATGGGGGAATTC CGAATCAGATGG TGTTCTGGGG GACAGGATCCTG GGTACGGCTCTG TTTGTGCTTGTG
 TACCCCTTAAG GCTTAGTCTACC ACAAGAGCCCC CTGTCTTAGGAC CCATGCCGAGAC AAACACGAACAC
 400 MetGlyGluPhe ArgIleArgTrp CysPheTrpGly AspArgIleLeu GlyThrAlaLeu PheValLeuVal
 1513 CTTATTCTTCTT CTTGGGAGGCTG AATATGCATCAG ACGACACTGCTC CGGCAACGGGCC AGTGTGGAGGCG
 GAATAAGAAGAA GAACCCCTCCGAC TTATACGTAGTC TGCTGTGACGAG GCCGTTGCCCGG TCACACCTCCGC
 424 LeuIleLeuLeu LeuGlyArgLeu AsnMetHisGln ThrThrLeuLeu ArgGlnArgAla SerValGluAla
 1585 GAAGCCGGCCAG CATGGTCCCCTG TGATAGGATTGA AAGAGCTACTGA GAATAGGGGGCT TCTCAATGAGAG
 CTTCCGCCGGTC GTACCAGGGGAC ACTATCCTAACT TTCTCGATGACT CTTATCCCCCGA AGAGTTACTCTC
 448 GluAlaGlyGln HisGlyProLeu (SEQ ID NO: 2)
 1657 AGCGGAGGCTGC TGTATCATGGG AACCAGGCAGAT CAATCATCCCTG GCAGGTCAGGCA GGAAGTTACTTA
 TCGCCTCCGACG ACAATAGTACCC TTGGTCCGTCTA GTTAGTAGGGAC CGTCCAGTCCGT CCTTCAATGAAT
 1729 GCTTCTCCTTCA CCTTCTTCCCAC AGAATTATTAT AGGCTTGTTCCA AGTTGTAGTGTG TGATCAGATTCTG
 CGAAGAGGAAGT GGAAGAAGGGTG TCTTAAATAATA TCCGAACAAGGT TCAACATCACAC ACTAGTCTAAGC
 1801 TGCTGCCCTGTCA GCTCTGTGCTAC CTGGCAGTTCCC CTCATGGAATTC GATATCAAGCTT ATCGATACCGTC
 ACGACGGACAGT CGAGACACGATG GACCGTCAAGGG GAGTACCTTAAG CTATAGTTGAA TAGCTATGGCAG
 1873 GACCT (SEQ ID NO: 1)
 CTGGA

FIG. 1C

FIG. 1A

FIG. 1B

FIG. 1C

FIG. 1

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1 GNTCTAGAANTA GTGGATCCCCC GGGCTGCAGGAA TTCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
CNAGATCTTNAT CACCTAGGGGG CCGACGTCCTT AAGGCTGCCGG GACCTTCCCGAG ACCACCCCGACT

73 GCGCTCTGCCG GGGGGCGGGC ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGCA TCAGCTACCGGG
CGCGAGACGGC CCCCCGCGCCG TGTCGTCCTTCG TCCAGGCGCACC CCGACCCCGCGT AGTCGATGGCCC

145 GTGGTCCGGCT GAAGAGCCAGGC AGCCAAGGCAGC CACCCCGGGGG TGGCGCACTTG GGGGAGTTGGTG
CACCAGGCCCGA CTTCTGGTCCG TCGGTTCCGTG GTGGGGCCCCC ACCCGCTGAAAC CCCCTCAACCAC

217 CCGCGCCCCCA GGCCTTGGCGG GTCATGGGCCC CCCATTCTGG CCGGGGGCGGTG CGAGTCGGGGCC
GGGGGGGGGT CCGGAACCGCCC CAGTACCCCGG GGGTAAGACCC GGGCCCCCGCAC GCTCAGCCCCGG
1 MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla

289 CTGCTGCTGCTG GGGTTTTGGG CTGGTGTCTGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
GACGACGACGAC CCCCCAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA

16 LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn

361 AAGAGGTTCCAG GCAGAGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
TTCTCCAAGGTC CGTCTCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG

40 LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro

433 CCGGCCCCGGCT CCTGGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGCTGTACCTG GTAGGGGGTGCT
GCCCGGGCCGGA GGACGGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA

64 ArgAlaArgPro ProGlyProHis SerSerProAsn TryGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505 CAGGGCCGGCGC TGTAGGCACCC CTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCA GACCTGGATCTC
GTCCCGGGCCGG AACTCCGTGGG GGACGGGGTTTG GAGGAAGAGTGA AACTAGCGGGT CTGGACCTAGAG

88 GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577 CGCTTCACCATC AAGTCCAGGAG TATAGCCCTAAT CTCCTGGGGCCAC GAGTCCGCTCG CACCACGATTAC
GCGAAGTGCTAG TTCAAGGTCTC ATATCGGGATTA GAGACCCCGGTG CTCAGGCGGAGC GTGGTGCTAATG

112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr

FIG. 2A

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649 TACATCATTGCC ACATCGGATGGG ACCGGGAGGGG CTGGAGAGCCTG CAGGAGGTGTG TGCCTAACAGAG
 136 ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
 TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg
 721 GGCATGAAGGTG CTTCTCCGAGTG GGACAAAGTCCC CGAGGAGGGGCT GTCCCCCGAAAA CCTGTGTCTGAA
 CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCCTCCCGA CAGGGGCTTTT GGACACAGACTT
 160 GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu
 793 ATGCCCCATGGAA AGAGACCGAGGG GCAGCCCCACAGC CTGGAGCCTGGG AAGAGAACCTG CCAGGTGACCCC
 TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTG GACCTCGGACCC TTCCTCTTGGAC GTCCACTGGGG
 184 MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro
 865 ACCAGCAATGCA ACCTCCCGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCCTGCA GTGGCTGGGGCA
 TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCGT
 208 ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla
 937 GCAGGGGGCTG GCGCTGCTCTTG CTGGCGTGGCA GGGGCTGGGGT GCCATGTGTTGG CGGAGACGGCGG
 CGTCCCCCGAC CGCGACGAGAAC GACCGCACCCGT CCGGACCCCA CCGTACACAACC GCCTCTGCCGCC
 232 AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg
 1009 GCCAAGCCTTCG GAGAGTCGCCAC CCTGGTCCITGG TCCTTCGGGAGG GGAGGGTCTCTG GGCTGGGGGGT
 CGGTTCCGGAAGC CTCTCAGCGGTG GGACCAGGACCG AGGAAGCCCTCC CTCCCAGAGAC CCGGACCCCCCA
 256 AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly
 1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGT GGCGGGGCTGCA
 CCTCCACCCTAC CCTGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
 280 GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla
 1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGG CATCCTGTGTAT ATCGTGCAGGAT
 CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCCCTA
 304 AspProProPhe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp
 1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACAAG GTATGAGGGCTC TTGGAGTGGCCC ATATTGCATACG
 CCGGGGGGGTTC TCGGGAGGTTTG TAGATGATGTTT CATACTCCCGAG AACCTCACCAGG TATAACGTATGC
 328 GlyProProGln SerProProAsn IleTyrTyrLys ValOP* (SEQ ID NO: 4)

FIG. 2B

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1297 AGCCCTTCTTGG GGTGCTCCTCCA GTTTAATTCCTG GTTTGAGGGACA CCTCTAACATCT CGGCCCCCTGTG
 TCGGAAGAACC CCACGAGAGGT CAATTAAGGAC CAACTCCCTGT GGAGATTGTAGA GCCGGGGGACAC

 1369 CCCCCCAGCCC CTTCACTCCTCC CGGCTGCTGTCC TCGTCTCCACTT TTAGGATTCTT AGGATTCCCACT
 GGGGGGTGGG GAAGTGAGGAG GCCGACGACAGG AGCAGAGGTGAA AATCCTAAGGAA TCCTAAGGGTGA

 1441 GCCCCACTTCCT GCCCTCCCGTT GGCCATGGGTGC CCCCCTCTGTCT CAGTGTCCCTGG ATCCTTTTCTCT
 CGGGTGAAGGA CGGAGGGGCAA CCGGTACCCACG GGGGAGACAGA GTCACAGGGACC TAGGAAAAAGGA

 1513 TGGGAGGGGCA CAGGCTCAGCCT CCTCTCTGACCA TGACCCAGGCAT CCTTGTCCCCCT CACCCACCCAGA
 ACCCTCCCCGT GTCCGAGTCGGA GGAGAGACTGGT ACTGGGTCCGTA GGAACAGGGGGA GTGGGTGGGTCT

 1585 GCTAGGGGCGGG AACAGCCACCT TTTGGTTGGCAC CGCCTTCTTTCT GCCTCTCACTGG TTTTCTCTTCTC
 CGATCCCCGCC TTGTGGGTGGA AAACCAACCGTG GCGGAAGAAAGA CCGAGAGTGACC AAAGAGAAGAG

 1657 TATCTCTTATTC TTTCCCTCTCTT CCGTCTCTAGGT CTGTTCTTCTTC CCTAGCATCCTC CTCCCCACATCT
 ATAGAGAATAAG AAAGGGAGAGAA GGCAGAGATCCA GACAAGAAGAAG GGATCGTAGGAG GAGGGTGTAGA

 1729 CCTTTCACCTC TTGGCTTCTTAT CCTGTGCCTCTC CCATCTCCTGGG TGGGGGCATCAA AGCATTTCTCCC
 GGAAAGTGGAG AACCGAAGAATA GGACACGGAGAG GGTAGAGGACCC ACCCCCGTAGTT TCGTAAAGAGGG

 1801 CTTAGCTTTCAG CCCCCCTTCTGA CCTCTCATACCA ACCACTCCCCCTC AGTCTGCCAAAA ATGGGGGCCCTTA
 GAATCGAAAGTC GGGGGGAAGACT GGAGAGTATGGT TGGTGAGGGGAG TCAGACGGTTTT TACCCCGGGAAT

 1873 TGGGGAAGGCTC TGACACTCCACC CCAGCTCAGGCC ATGGGCACCAGG GCTCCATTCTCT GGCCTGGCCCCAG
 ACCCTTCCGAG ACTGTAGGGTGG GGTGAGTCCGG TACCCGTCGTCC CGAGGTAAGAGA CCGGACCGGGTC

 1945 GCCTCTACATAC TTACTCCAGCCA TTTGGGTGGTT GGGTCATGACAG CTACCATGAGAA GAAGTGTCCCGT
 CGGAGATGTATG AATGAGTCCGT AAACCCCAACCA CCCAGTACTGTC GATGGTACTCTT CTTACAGGGCA

 2017 TTTGTCCSGTGG CCAATAGCAAGA TATGAACCGGTC GGGACATGTATG GACTTGGTCTGA TGCTGAATGGGC
 AACAGGTCACC GGTATCGTTCT ATACTTGGCCAG CCCTGTACATAC CTGAACAGACT ACGACTTACCCG

FIG. 2C

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2089 CACTTGGACCG GAAGTGACTTGC TCCAGACAAGAG GTGACCAGGCCG GGACAGAAATGG CCTGGGAAGTAG
GTGAACCCCTGGC CTTCACTGAACG AGGTCTGTTCTC CACTGGTCCGGG CCTGTCTTTACC GGACCCCTTCATC

2161 CAGAAGCAGTGC AGCAGGAACTGG AAGTGCCCTTCAT CCAGGACAGGAA GTAGCACTTCTG AAACAGGGAAGTG
GTCTTCGTCACG TCGTCCCTTGACC TTCACGGAAGTA GGTCCTGTCTT CATCGTGAAGAC TTTGTCTTTCAC

2233 GTCTGGCTGGAA CTCCAAGTGGCT TAGTCTGGGGGA TCAGGAGGTGGG AGGTGGATGGT CTTATTCTGTGG
CAGACCGACCTT GAGGTTCAACCGA ATCAGACCCCTT AGTCTCCACCC TCCACCTACCAA GAATAAGACACC

2305 AGAAGAAGGGCG GGAAGAAGTCTCC TTTCAGGAGGAA GCTGGAACCTTAC TGACTGTAAGAG GTTAGAGGTGGA
TCTTCTTCCCGC CCTTCTTGAAGG AAAGTCCCTCCT CGACCTTGAATG ACTGACATTCTC CAATCTCCACCT

2377 CCGA (SEQ ID NO: 3)
GGCT

FIG. 2D

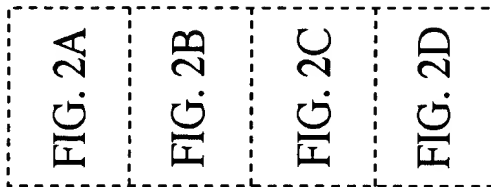


FIG. 2

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AL-2b.L	1	GNTCTAGAA	NTAGTGGAT	CCCCCGGGCT	GCAGGAAT	TCCGACGGCCCCCT
AL-2b.L	51	GGAAGGGCT	CTGGTGGGGCT	GAGCGCTCT	GCCGCGGGGCGCGGCACAG	
AL-2b.L	101	CAGGAAGC	AGGTCCGCGT	GGGCGCTGGGGCA	TACGTACCGGGGTGGTC	
AL-2b.L	151	CGGGCTGA	AGAGCCAGGC	AGCCAGCCAGCCG	GGGGGTGGGCGAC	
AL-2b.L	201	TTTGGGGAG	TTGGTGCCCG	CCCGCAGGCC	TTGGCGGGTCA	TGGGGC
AL-2b.L	251	CCCCCATT	CTGGCCGGGG	CGTGCGAGT	CGGGCCCTGCTGCTGCTG	
AL-2b.L	301	GGGGTTT	TGGGCTGGT	CTGGGCTCAGCC	TGGAGCCTGTCTACTGGA	
AL-2b.L	351	CTCGGCGA	ATAAGAGGT	TCCAGGCAGAGG	TGGTTATGTGCTGTACCCCTC	
AL-2b.L	401	AGATCGGG	GACCGGCTAG	ACCTGCTCTGCC	CCCGGGCCTCCTGGC	
AL-2b.L	451	CCTCACTC	CTCCTAATTA	TGAGTTCTACA	AGCTGTACCTGGTAGGGGG	
AL-2b.L	501	TGCTCAGG	GCCGG	CGCTGTGAGG	CACCCCTGCCCCCAACCTCCTCTCA	
HI0006	1	- - - - -	GCCGA	CGCTGTGAGG	CACCCCTGCCCCCAACCTCCTCTCA	
AL-2b.L	551	CTTGTGAT	CGCCCA	GACCTGGATCT	CCGCTTCACCATCAAGTTCCAGGAG	
HI0006	43	CTTGTGAT	CGCCCA	GACCTGGATCT	CCGCTTCACCATCAAGTTCCAGGAG	
AL-2b.L	601	TATAGCCC	TAACTCT	CTGGGCCACGAGT	TCCGCTCGCACCAAGTTACTA	
HI0006	93	TATAGCCC	TAACTCT	CTGGGCCACGAGT	TCCGCTCGCACCAAGTTACTA	
AL-2b.L	651	CATCAT	TGCCACAT	CGGATGGGAC	CCCGGAGGGCTGGAGAGCCTGCAGG	
HI0006	143	CATCAT	TGCCACAT	CGGATGGGAC	CCCGGAGGGCTGGAGAGCCTGCAGG	
AL-2b.L	701	GAGGTGTG	TGCCATA	ACCAGAGGCAT	GAGGTGCTTCTCCGAGTGGGACAA	
HI0006	193	GAGGTGTG	TGCCATA	ACCAGAGGCAT	GAGGTGCTTCTCCGAGTGGGACAA	

FIG. 3A

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AL-2b.L 751 AGT C C C C G A G G G G C T G T C C C C C G A A A A C C T G T G T C T G A A A T G C C C C A T
H10006 243 AGT - C C C G A G G G G C T G T C C C C C G A A A A C C T G T G T C T G A A A T G C C C C A T

AL-2b.L 801 G G A A A G A G A C C G A G G G G C A G C C C A C A G C C T - G G A G C C T - G G G A A G G A G A A
H10006 292 G G A A A G A G A C C G A G G G G C A G C C C A C A G C C T G G G A G C C T G G G G A A G G A G A A

AL-2b.L 849 C C T G C C A G G T G A C C C C A C C A G C A A T G C A A C C T C C C G G G T - - G C T G A A A G G
H10006 342 C C T G C C A G G T G A C C C C A C C A G C A A T N C A A C C T T C C G G G G T T G C T T G A A G G

AL-2b.L 897 C C C C C T - - G C C C C C C T C C C C A G C A - T G C C C T G C A G T - - G G C T G G G G C A G C A G G
H10006 392 G C C C C T T G A C C C T T T C C C A G C A T T G C N T G C A N T T G G T T N G G G G C A G C A N G

AL-2b.L 942 G G G G C - - - T G G C G C T G C T C T T G C T G G G C G T G G C A G G G G C T G G G G G T G C C
H10006 442 G G G G N G T T T T G G C (SEQ ID NO: 5)

AL-2b.L 988 A T G T G T T G C G G A G A C G G C G G G C C A A G C C T T C G G A G A G T C G C C A C C C T G G

AL-2b.L 1038 T C C T G G C T C C T T C G G G A G G G A G G T C T C T G G C C T G G G G G T G G A G G T G

AL-2b.L 1088 G G A T G G G A C C T C G G G A G G C T G A G C C T G G G G A G C T A G G G A T A G C T C T G C G G

AL-2b.L 1138 G G T G G C G G G C T G C A G A T C C C C C C T T C T G C C C C A C T A T G A G A A G G T G A G

AL-2b.L 1188 T G G T G A C T A T G G G C A T C C T G T G T A T A T C G T G C A G G A T G G G C C C C C C A G A

AL-2b.L 1238 G C C C T C C A A C A T C T A C A C A T C G A T T T C T G T G T T G G A G T G G C C C A T A

AL-2b.L 1288 T T G C A T A C G A T A C A A C T G T T T T T C A T G C G A T C C A A G T G C T C C C G T G T C A C

FIG. 3B



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AL-2b.L1338 T A C A T T C T T A T T T C C T G T G C A A G T T A T T A C G A C A T C G A C T T G C C G G A T G A
AL-2b.L1388 C T T C A T T T A G C T T T A C G A C C C T G A A C C C A T C C A T G C A G G C C T G C A G A G C A
AL-2b.L1438 C A G A T G G G G A A T T C C G A A T C A G A T G G T G T T T C T G G G G G A C A G G A T C C T
AL-2b.L1488 G G G T A C G G C T C T G T T T G T G C T T G T G C T T A T T C T T C T T G G G A G G C T G A
AL-2b.L1538 A T A T G C A T C A G A C G A C A G T G C T C C G G C A A C G G G C C A G T G T G G A G G C G G A A
AL-2b.L1588 G C C G G C C A G C A T G G T C C G C T G T G A T A G G A T T G A A A G A G C T A C T G A G A A T A
AL-2b.L1638 G G G G G C T T C T C A A T G A G A G A G C G G A G G C T G C T G T T A T C A T G G G A A C C A G G
AL-2b.L1688 C A G A T C A A T C A T C C C T G G C A G Q T C A G G C A G G A A G T T A C T T A G C T T C T C C T
AL-2b.L1738 T C A C C T T C T T C C C A C A G A A T T A T T A T A G G C T T G T T C C A A G T T G T A G T G T
AL-2b.L1788 G T G A T C A G A T T C G T G C T G C C T G T C A G C T C T G T G C T A C C T G G C A G T T C C C C
AL-2b.L1838 T C A T G G A A T T C G A T A T C A A G C T T A T C G A T A C C G T C G A C C T (SEQ ID NO: 1)

FIG. 3C

FIG. 3A
FIG. 3B
FIG. 3C

FIG. 3

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lerk2 1 MA - RP GQRWLGKWL VAMV VWA L CRLATPLAKNLEPVSWSLNPKFLSGKG
 huHTKL 1 MAVRRDSVWVKYCWGLMV - - - LCRTAISKSIVLEPIYWNSSNSKFLPGQG
 AL2.sht 1 MG - PPHSGPGGVRVGALLLGVLGLVSGL - - - SLEPVYWN SANKRFQAE EG
 AL2.long 1 MG - PPHSGPGGVRVGALLLGVLGLVSGL - - - SLEPVYWN SANKRFQAE EG

lerk2 50 LV IYPKIGDKLDIICPRA - - - EAGR - - - PYEYKLYLV RPEQAACSTVLD
 huHTKL 48 LVLYPQIGDKLDIICPKV - - - DSKTVGQY EYK[V]YV D K D Q A D R C T I K K E
 AL2.sht 48 YVLYPQIGDRLD LCPRARPPGPHSSPNYEFYKLYLVGGAGRRCEAPPA
 AL2.long 48 YVLYPQIGDRLD LCPRARPPGPHSSPNYEFYKLYLVGGAGRRCEAPPA

lerk2 95 PNVLVTCNRP E Q EIRFTIKFQEFSPN Y M G L E F K K H H D Y Y I T S T S N G S L E G
 huHTKL 95 NTPLLNCAKPDQDIKFTIKFQEFSPNLWG L E F Q K N K D Y Y I I S T S N G S L E G
 AL2.sht 98 PNL L L T C D R P D L D L R F T I K F Q E Y S P N L W G H E F R S H D Y Y I I A T S D G T R E G
 AL2.long 98 PNL L L T C D R P D L D L R F T I K F Q E Y S P N L W G H E F R S H D Y Y I I A T S D G T R E G

lerk2 145 LENREGGVCRTTRTMK IIMKVGGQDPNAVTP EQLTTSRPSKEADNTVKMATQ
 huHTKL 145 LDNREGGVCQTRAMKILMKVGQDASS - - - - - AGSTRNKDPTRRPELEAG
 AL2.sht 148 LESLQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSLE
 AL2.long 148 LESLQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSLE

FIG. 4A

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lerk2 195 A P G S R G S L G D S D G K H E T V N Q E E K S G P G A S G G S S G D P D G F F N S K V A L F A A V
huHTKL 189 T N G - R S S T T S P F V K P N P G S S T D G N S A G H S G - - - - - N N I L G S E V A L F A G I
AL2.sht 198 - P G K E N L P G D P T S N A T S R G A E G P L P P S M P A V A G A A G G L - - - A L L L L G V A
AL2.long 198 - P G K E N L P G D P T S N A T S R G A E G P L P P S M P A V A G A A G G L - - - A L L L L G V A

lerk2 245 G A G C V I F L L I I I F L T V L L L K L R K R H R K H T Q - Q R A A A L S L S T L A S P K G G S G
huHTKL 232 A S G C I I F I V I I I T L V V L L L K Y R R R H R K H S P - Q H T T T L S L S T L A T P K R S G N
AL2.sht 244 G A G G A - - - - - M C W R R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - - G G G M G
AL2.long 244 G A G G A - - - - - M C W R R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - - G G G M G

lerk2 294 T A G T E P S D I I I P L R - - - T T E N N Y C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S P A
huHTKL 261 N N G S E P S D I I I P L R - - - T A D S V F C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S P A
AL2.sht 265 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S P P
AL2.long 295 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S P P

lerk2 341 N I Y Y -
huHTKL 328 N I Y Y -
AL2.sht 335 N I Y Y -
AL2.long 335 N I Y Y T S I S V L E W P I L H T I Q L F F M R S K C S R V T T F L F P V Q V I T T S T C R M T S F

FIG. 4B

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lerk2	345	- - - - -	- - - - -	KV	(SEQ ID NO: 9)
huHTKL	332	- - - - -	- - - - -	KV	(SEQ ID NO: 10)
AL2.sht	339	- - - - -	- - - - -	KV	(SEQ ID NO: 4)
AL2.long	385	S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L N M H			

AL2.long 435 Q T T L L R Q R A S V E A E A G Q H G P L (SEQ ID NO: 2)

FIG. 4C

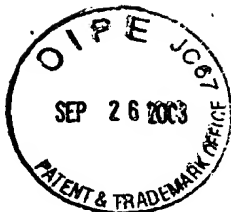
FIG. 4A

FIG. 4B

FIG. 4C

FIG. 4





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LERK2 1 MA-RPGQRWLSKWLAMVVLTLCLRLATPLAKNLLEPVSWSSLNPKFLSGKG
huHTKL 1 MAVRRDSVWKYCMGVLMLV---LCRTAISKSI VLEPIYWNSSNSKFLPGQG
AL2.long 1 MGPPHSGP-GGVRVGA LLL--LGVLLGLVSGLSLEPVYWNSSANKRFQAEQG

LERK2 50 LVIYPKIGDKLDIICPRA---EAGR--PYEY YKLYLV RPEQAACSTVLD
huHTKL 48 LVLYPQIGDKLDIICPKV---DSKT VGGY EY YKVMV D KDAQADRC TIKKE
AL2.long 48 YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAGQRRC EAPPA

LERK2 95 PNVLVTCTNKP HQEIRFTIKFQEFSPNYMGL EFKYH DYYITSTN SGL EG
huHTKL 95 NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTN SGL EG
AL2.long 98 PNLLLTCDRPLDLLRFTIKFQEYSPNLWGHEFRSHH DYYIIATSDGTREG

LERK2 145 LENREGGVCRTTRTMKIVMKVGQDPNAVTP EQLTTSRPSKESDNTVKTATQ
huHTKL 145 LDNQEGGVCQTRAMKILMKVGQDASS-----AGSTRNKDPTRRPELEAG
AL2.long 148 LESLQGGVC LTRGMKVLRLRVGQS PRG-----GAVPRKPVS E MPMERDRG

huHTKL 195 APGRGSQGDSDGKHETVNQEEKSGPGAGGGSGDSDSFFNSKV ALFAVAG
AL2.sht 189 TNGRSS TTS PFVKPNPGSSSTDGNSAGHSG-----NNILGSEVALFAGIA
AL2.long 192 AHSLEPGKENLP G DPTSNATSRGA E-----GPLPPSPMPAVAGAA

FIG. 5A



LERK2 292 - **G**TA**G**TEPSDIIIPLR - - - TTENNYCPHYEKVSGDYGHPVYI VQEMP PQS

huHTKL 280 - NNN**G**SEPSDIIIPLR - - - TADSVFCPHYEKVSGDYGHPVYI VQEMP PQS

AL2.long283 M**G**PREAEP**G**ELGIALRGGAADPPFCPHYEKVSGDYGHPVYI VQ**D**GP PQS

LERK2	344	- - - - -	- - - - -	- - - - -	K V	(SEQ ID NO: 9)
huHTKL	332	- - - - -	- - - - -	- - - - -	K V	(SEQ ID NO: 10)
AL2.long	383	S F S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L G R L N				

AL2.long433 MHQ T T L L R Q R A S V E A E A G Q H G P L (SEQ ID NO:2)

FIG. 5B

FIG. 5